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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Tue Oct 30 17:50:12 EDT 2007

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Application No: 10520655 Version No: 2.0

Input Set:

Output Set:

Started: 2007-10-09 12:57:55.239
Finished: 2007-10-09 12:58:00.579
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 340 ms
Total Warnings: 17
Total Errors: 30
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)

Input Set:

Output Set:

Started: 2007-10-09 12:57:55.239
Finished: 2007-10-09 12:58:00.579
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 340 ms
Total Warnings: 17
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Actual SeqID Count: 18

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
E 257	Invalid sequence data feature in <221> in SEQ ID (14)
E 257	Invalid sequence data feature in <221> in SEQ ID (14)
E 257	Invalid sequence data feature in <221> in SEQ ID (14) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)

SEQUENCE LISTING

<110> DIDEBERG, OTTO
VERNET, THIERRY
MOUZ, NICOLAS

<120> STREPTOCOCCUS PNEUMONIAE PBP2X MINI-PROTEIN AND USES
THEREOF

<130> 70457-19

<140> 10520655
<141> 2005-03-07

<150> PCT/IB03/003397
<151> 2003-07-11

<150> FR 02/08724
<151> 2002-07-11

<160> 18

<170> PatentIn Ver. 3.3

<210> 1
<211> 551
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
mini-PBP2x construct

<400> 1

Gly Ser Gly Ala Lys Arg Gly Thr Ile Tyr Asp Arg Asn Gly Val Pro
1 5 10 15

Ile Ala Glu Asp Ala Thr Ser Gly Gly Pro Asn Arg Ser Tyr Pro Asn
20 25 30

Gly Gln Phe Ala Ser Ser Phe Ile Gly Gly Met Glu Ser Ser Leu
35 40 45

Asn Ser Ile Leu Ala Gly Gly Asp Gly Lys Asp Val Tyr Thr
50 55 60

Thr Ile Ser Ser Pro Leu Gln Ser Phe Met Glu Thr Gln Met Asp Ala
65 70 75 80

Phe Gln Glu Lys Val Lys Gly Lys Tyr Met Thr Ala Thr Leu Val Ser
85 90 95

Ala Lys Thr Gly Glu Ile Leu Ala Thr Thr Gln Arg Pro Thr Phe Asp
100 105 110

Ala Asp Thr Lys Glu Gly Ile Thr Glu Asp Phe Val Trp Arg Asp Ile

	115	120	125
Leu Tyr Gln Ser Asn Tyr Glu Pro Gly Ser Thr Met Lys Val Met Met			
130	135	140	
Leu Ala Ala Ala Ile Asp Asn Asn Thr Phe Pro Gly Gly Glu Val Phe			
145	150	155	160
Asn Ser Ser Glu Leu Lys Ile Ala Asp Ala Thr Ile Arg Asp Trp Asp			
165	170	175	
Val Asn Glu Gly Leu Thr Gly Gly Arg Met Met Thr Phe Ser Gln Gly			
180	185	190	
Phe Ala His Ser Ser Asn Val Gly Met Thr Leu Leu Glu Gln Lys Met			
195	200	205	
Gly Asp Ala Thr Trp Leu Asp Tyr Leu Asn Arg Phe Lys Phe Gly Val			
210	215	220	
Pro Thr Arg Phe Gly Leu Thr Asp Glu Tyr Ala Gly Gln Leu Pro Ala			
225	230	235	240
Asp Asn Ile Val Asn Ile Ala Gln Ser Ser Phe Gly Gln Gly Ile Ser			
245	250	255	
Val Thr Gln Thr Gln Met Ile Arg Ala Phe Thr Ala Ile Ala Asn Asp			
260	265	270	
Gly Val Met Leu Glu Pro Lys Phe Ile Ser Ala Ile Tyr Asp Pro Asn			
275	280	285	
Asp Gln Thr Ala Arg Lys Ser Gln Lys Glu Ile Val Gly Asn Pro Val			
290	295	300	
Ser Lys Asp Ala Ala Ser Leu Thr Arg Thr Asn Met Val Leu Val Gly			
305	310	315	320
Thr Asp Pro Val Tyr Gly Thr Met Tyr Asn His Ser Thr Gly Lys Pro			
325	330	335	
Thr Val Thr Val Pro Gly Gln Asn Val Ala Leu Lys Ser Gly Thr Ala			
340	345	350	
Gln Ile Ala Asp Glu Lys Asn Gly Gly Tyr Leu Val Gly Leu Thr Asp			
355	360	365	
Tyr Ile Phe Ser Ala Val Ser Met Ser Pro Ala Glu Asn Pro Asp Phe			
370	375	380	
Ile Leu Tyr Val Thr Val Gln Gln Pro Glu His Tyr Ser Gly Ile Gln			
385	390	395	400
Leu Gly Glu Phe Ala Asn Pro Ile Leu Glu Arg Ala Ser Ala Met Lys			
405	410	415	
Asp Ser Leu Asn Leu Gln Thr Thr Ala Lys Ala Leu Glu Gln Val Ser			

420	425	430
Gln Gln Ser Pro Tyr Pro Met Pro Ser Val Lys Asp Ile Ser Pro Gly		
435	440	445
Asp Leu Ala Glu Glu Leu Arg Arg Asn Leu Val Gln Pro Ile Val Val		
450	455	460
Gly Thr Gly Thr Lys Ile Lys Asn Ser Ser Ala Glu Glu Gly Lys Asn		
465	470	475
Leu Ala Pro Asn Gln Gln Val Leu Ile Leu Ser Asp Lys Ala Glu Glu		
485	490	495
Val Pro Asp Met Tyr Gly Trp Thr Lys Glu Thr Ala Glu Thr Leu Ala		
500	505	510
Lys Trp Leu Asn Ile Glu Leu Glu Phe Gln Gly Ser Gly Ser Thr Val		
515	520	525
Gln Lys Gln Asp Val Arg Ala Asn Thr Ala Ile Lys Asp Ile Lys Lys		
530	535	540
Ile Thr Leu Thr Leu Gly Asp		
545	550	

<210> 2
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 2
gtcgacttag tctcctaaag ttaatttaat ttttttaatg tttttg 46

<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 3
ggatccggga caggcactcg c 21

<210> 4
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 4
cataaatagt cccacgttg gccccggatc cacgcggaac cag 43

<210> 5
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 5
gtttggtaa ctacgattgg gacctccaga gggtgcattcc tcagcaatcg g 51

<210> 6
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 6
gttcaaggaa ctctccattc caccggcgat aaaactagaa gcaaattg 48

<210> 7
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 7
tgtataaaca tccttaccgt ccccacctcc ccctgcaaga atactgttc 49

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 8
ccgcatatgg ccaaacgtgg gactattat

<210> 9
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 9
ggctcgagtt agtctcctaa agttaatgtat

<210> 10
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (4)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (5)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (6)
<223> Asp or Ser

<220>
<221> MOD_RES
<222> (10)..(12)
<223> variable amino acid

<400> 10
Arg Gly Xaa Xaa Xaa Xaa Arg Ser Gly Xaa Xaa Xaa Ala
1 5 10

30

<210> 11

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (2)..(3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (5)
<223> variable amino acid

<400> 11
Xaa Xaa Xaa Pro Xaa Gly
1 5

<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)
<223> Gly or Tyr

<220>
<221> MOD_RES
<222> (2)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (4)..(6)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (8)..(9)
<223> variable amino acid

<400> 12
Xaa Xaa Glu Xaa Xaa Xaa Asp Xaa Xaa Leu
1 5 10

<210> 13
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (2)..(3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (4)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (5)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (7)..(9)
<223> variable amino acid

<400> 13
Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Gln
1 5 10

<210> 14
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (2)
<223> Gly or Ser

<220>
<221> MOD_RES
<222> (4)..(5)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (6)..(9)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (12)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (13)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (14)
<223> Asp or Asn

<400> 14
Thr Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Ser Pro Xaa Xaa Xaa
1 5 10

<210> 15
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (1)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (4)
<223> Ala or Gly

<220>
<221> MOD_RES
<222> (6)..(7)
<223> variable amino acid

<400> 15
Xaa Glu Pro Xaa Ser Xaa Xaa Lys

<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)
<223> hydrophobic amino acid

<220>
<221> MOD_RES
<222> (2)..(3)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (5)
<223> variable amino acid

<220>
<221> MOD_RES
<222> (7)
<223> hydrophobic amino acid

<400> 16
Xaa Xaa Xaa Ser Xaa Asn Xaa
1 5

<210> 17
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 17
Ala Lys Arg Gly Thr Ile Tyr
1 5

<210> 18
<211> 750
<212> PRT
<213> Streptococcus pneumoniae

<400> 18

Met Lys Trp Thr Lys Arg Val Ile Arg Tyr Ala Thr Lys Asn Arg Lys
1 5 10 15

Ser Pro Ala Glu Asn Arg Arg Arg Val Gly Lys Ser Leu Ser Leu Leu
20 25 30

Ser Val Phe Val Phe Ala Ile Phe Leu Val Asn Phe Ala Val Ile Ile
35 40 45

Gly Thr Gly Thr Arg Phe Gly Thr Asp Leu Ala Lys Glu Ala Lys Lys
50 55 60

Val His Gln Thr Thr Arg Thr Val Pro Ala Lys Arg Gly Thr Ile Tyr
65 70 75 80

Asp Arg Asn Gly Val Pro Ile Ala Glu Asp Ala Thr Ser Tyr Asn Val
85 90 95

Tyr Ala Val Ile Asp Glu Asn Tyr Lys Ser Ala Thr Gly Lys Ile Leu
100 105 110

Tyr Val Glu Lys Thr Gln Phe Asn Lys Val Ala Glu Val Phe His Lys
115 120 125

Tyr Leu Asp Met Glu Glu Ser Tyr Val Arg Glu Gln Leu Ser Gln Pro
130 135 140

Asn Leu Lys Gln Val Ser Phe Gly Ala Lys Gly Asn Gly Ile Thr Tyr
145 150 155 160

Ala Asn Met Met Ser Ile Lys Lys Glu Leu Glu Ala Ala Glu Val Lys
165 170 175

Gly Ile Asp Phe Thr Thr Ser Pro Asn Arg Ser Tyr Pro Asn Gly Gln
180 185 190

Phe Ala Ser Ser Phe Ile Gly Leu Ala Gln Leu His Glu Asn Glu Asp
195 200 205

Gly Ser Lys Ser Leu Leu Gly Thr Ser Gly Met Glu Ser Ser Leu Asn
210 215 220

Ser Ile Leu Ala Gly Thr Asp Gly Ile Ile Thr Tyr Glu Lys Asp Arg
225 230 235 240

Leu Gly Asn Ile Val Pro Gly Thr Glu Gln Val Ser Gln Arg Thr Met
245 250 255

Asp Gly Lys Asp Val Tyr Thr Thr Ile Ser Ser Pro Leu Gln Ser Phe
260 265 270

Met Glu Thr Gln Met Asp Ala Phe Gln Glu Lys Val Lys Gly Lys Tyr
275 280 285

Met Thr Ala Thr Leu Val Ser Ala Lys Thr Gly Glu Ile Leu Ala Thr
290 295 300

Thr Gln Arg Pro Thr Phe Asp Ala Asp Thr Lys Glu Gly Ile Thr Glu
305 310 315 320

Asp Phe Val Trp Arg Asp Ile Leu Tyr Gln Ser Asn Tyr Glu Pro Gly
325 330 335

Ser Thr Met Lys Val Met Met Leu Ala Ala Ala Ile Asp Asn Asn Thr
340 345 350

Phe Pro Gly Gly Glu Val Phe Asn Ser Ser Glu Leu Lys Ile Ala Asp
355 360 365

Ala Thr Ile Arg Asp Trp Asp Val Asn Glu Gly Leu Thr Gly Gly Arg
370 375 380

Met Met Thr Phe Ser Gln Gly Phe Ala His Ser Ser Asn Val Gly Met
385 390 395 400

Thr Leu Leu Glu Gln Lys Met Gly Asp Ala Thr Trp Leu Asp Tyr Leu
405 410 415

Asn Arg Phe Lys Phe Gly Val Pro Thr Arg Phe Gly Leu Thr Asp Glu
420 425 430

Tyr Ala Gly Gln Leu Pro Ala Asp Asn Ile Val Asn Ile Ala Gln Ser
435 440 445

Ser Phe Gly Gln Gly Ile Ser Val Thr Gln Thr Gln Met Ile Arg Ala
450 455 460

Phe Thr Ala Ile Ala Asn Asp Gly Val Met Leu Glu Pro Lys Phe Ile
465 470 475 480

Ser Ala Ile Tyr Asp Pro Asn Asp Gln Thr Ala Arg Lys Ser Gln Lys
485 490 495

Glu Ile Val Gly Asn Pro Val Ser Lys Asp Ala Ala Ser Leu Thr Arg
500 505 510

Thr Asn Met Val Leu Val Gly Thr Asp Pro Val Tyr Gly Thr Met Tyr
515 520 525

Asn His Ser Thr Gly Lys Pro Thr Val Thr Val Pro Gly Gln Asn Val
530 535 540

Ala Leu Lys Ser Gly Thr Ala Gln Ile Ala Asp Glu Lys Asn Gly Gly
545 550 555 560

Tyr Leu Val Gly Leu Thr Asp Tyr Ile Phe Ser Ala Val Ser Met Ser
565 570 575

Pro Ala Glu Asn Pro Asp Phe Ile Leu Tyr Val Thr Val Gln Gln Pro
580 585 590

Glu His Tyr Ser Gly Ile Gln Leu Gly Glu Phe Ala Asn Pro Ile Leu
595 600 605

Glu Arg Ala Ser Ala Met Lys Asp Ser Leu Asn Leu Gln Thr Thr Ala
610 615 620

Lys Ala Leu Glu Gln Val Ser Gln Gln Ser Pro Tyr Pro Met Pro Ser
625 630 635 640

Val Lys Asp Ile Ser Pro Gly Asp Leu Ala Glu Glu Leu Arg Arg Asn
645 650 655

Leu Val Gln Pro Ile Val Val Gly Thr Gly Thr Lys Ile Lys Asn Ser
660 665 670

Ser Ala Glu Glu Gly Lys Asn Leu Ala Pro Asn Gln Gln Val Leu Ile
675 680 685

Leu Ser Asp Lys Ala Glu Glu Val Pro Asp Met Tyr Gly Trp Thr Lys
690 695 700

Glu Thr Ala Glu Thr Leu Ala Lys Trp Leu Asn Ile Glu Leu Glu Phe
705 710 715 720

Gln Gly Ser Gly Ser Thr Val Gln Lys Gln Asp Val Arg Ala Asn Thr
725 730 735

Ala Ile Lys Asp Ile Lys Lys Ile Thr Leu Thr Leu Gly Asp
740 745 750